

Tue Aug 28 11:09:18 2001

us-09-486-334-2.rsp

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: August 21, 2001, 12:06:43 ; Search time 11.18 Seconds
(without alignments)
962.095 Million cell updates/sec

Title: us-09-486-334-2
Perfect score: 1641
Sequence: 1 MATCIDTCRTGNTODDSRF.....IPCLINDQSYLEMSDYVI 314
Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 3425486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	648.5	39.5	273	1	CYSE_ECOLI
2	648.5	39.5	273	1	CYSE_SALTY
3	624.5	38.1	267	1	CYSE_HAEM
4	573.5	34.9	274	1	CYSE_BUCAL
5	549.5	33.5	261	1	CYSE_BUCAP
6	430.5	26.2	244	1	CYSE_SYN7
7	424	25.8	217	1	CYSE_BACSU
8	420.5	25.6	249	1	CYSE_SYNY3
9	399	24.3	216	1	CYSE_STAXY
10	369.5	22.5	269	1	NIIP_AZOCH
11	365	22.2	171	1	CYSE_HELPJ
12	359	21.9	171	1	CYSE_HELPJ
13	287	17.5	319	1	SRPH_SYN7
14	217	13.2	162	1	WCAB_ECOLI
15	164.5	10.0	190	1	NODL_RHIV
16	164.5	10.0	214	1	YAG4_METUA
17	160	9.8	203	1	THGA_ECOLI
18	156.5	9.5	196	1	YJY8_YEAST
19	153.5	9.4	207	1	YAO3_SCHPO
20	150	9.1	183	1	NODL_RHME
21	146.5	8.9	346	1	LPXD_RICPR
22	136.5	8.3	184	1	MAA_BACSU
23	133.5	8.1	345	1	LPXD_RICRI
24	127.5	7.9	182	1	MAA_ECOLI
25	127.5	7.8	261	1	LPXA_AQUAE
26	127.5	7.7	276	1	TABP_PBSB2
27	126.5	7.7	172	1	CAPG_STPAU
28	120.5	7.3	207	1	THGA_LACIA
29	120	7.3	159	1	Y304_METUA
30	117.5	7.2	182	1	WCAB_ECOLI
31	115.5	7.0	267	1	LPXA_PROMI
32	115	7.0	262	1	LPXA_HAEM
33	114.5	7.0	262	1	LPXA_YEREN

RESULT	ID	STANDARD	PRT
34	112.5	6.9	456
35	112	6.8	116
36	112	6.8	456
37	110	6.7	209
38	110	6.6	456
39	106.5	6.5	340
40	105.5	6.4	171
41	104.5	6.4	275
42	103.5	6.3	209
43	103	6.3	210
44	103	6.3	210
45	102.5	6.2	210

ALIGNMENTS

RESULT 1
ID CYSE_ECOLI STANDARD PRT: 273 AA.
AC P05796:
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DI 30-MAY-2000 (Rel. 39, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT)
GN CYSE:
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
NCBI_TaxID=562;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=8009872; PubMed=3309158;
RA Deak D., Boeck A.;
RT "L-cysteine biosynthesis in Escherichia coli: nucleotide sequence and expression of the serine acetyltransferase (cysE) gene from the wild-type and a cysteine-excreting mutant."
RT J. Gen. Microbiol. 133:515-525(1987).
RN
RP [2]
RX SEQUENCE FROM N.A.
RA STRAIN-K12;
RT MEDLINE=90211342; PubMed=2108679;
RA Tel H., Murata K., Kimura A.;
RT "Structure and expression of cysX, the second gene in the Escherichia coli K-12 cysE locus."
RN
RP Biochem. Biophys. Res. Commun. 167:948-955(1990).
RN
RP [3]
RX STRAIN-K12 / MG1655;
RA MEDLINE=94316500; PubMed=8041620;
RT Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes."
RN
RP Nucleic Acids Res. 22:2576-2586(1994).
RN
RP [4]
RX CHARACTERIZATION;
RA MEDLINE=91099514; PubMed=2125278;
RT Wigley D.B., Derrick J.P., Shaw W.V.;
RT "The serine acetyltransferase from Escherichia coli: over-expression, purification and preliminary crystallographic analysis."
RN
RP FEBS Lett. 277:267-271(1990).
RN
RP SUBUNIT;
RX MEDLINE=20085066; PubMed=10617639;
RA Haddon V.J., Moody P.C., Rowe A.J., Shaw W.V.;
RT "Serine acetyltransferase from Escherichia coli is a dimer of trimers."
RN
RX J. Biol. Chem. 275:461-466(2000).
RT "CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE -> CoA + O-ACETYL-L-SERINE."
CC -1- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER. DIMER OF A HOMODIMER.

P14192 bacillus su
P42817 bacillus ca
P17114 escherichia
P50870 enterococu
P43889 haemophilus
P18482 salmoneila
P43888 haemophilus
O85290 buchnera ap
P45284 haemophilus
P23364 agrobacteri
P26828 escherichia
P50869 morganella

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC
 DR EMBL: M15745; AAA33648.1;
 DR EMBL: M34333; AAA23659.1;
 DR EMBL: U00039; AAB18584.1;
 DR PIR: A27896; XECSA.
 DR PIR: A34563; A34563.
 DR ECODBASE: H029.3; 6TH EDITION.
 DR Ecogene: EGI0187; CYSE.
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep. 2.
 DR PROSITE: PS00101; HEXAPEP-TRANSFERASES; 1.
 DR Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
 KW SEQUENCE 273 AA; 29316 MW; 466EB98750E709 CRC64;
 SQ

Query Match
 Best Local Similarity 39.5%; Score 648.5; DB 1; Length 273;
 Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;

DB 4 EELEIYWNKIKAEKADVKOEPIISNYVYASITSHRSLSALAHILSVKLSNLPNTL 102
 QY 103 FELFIVLEESSEITESTKODLAVKERDPACISYHCEFLGKFGFLACQARHATHTLMO 63
 DB 64 REVEEAVAADEPMASACDIOAVTRDPADVAKYSTPLLYLKFFHALQVYRGHMLNK 162
 QY 163 NRKIYALLIQNRSEFAVDIHGKATIGKGLLDHAGVVGTAAGVNDVSTLHGVTG 123
 DB 124 GRALALFQNOVSFQVDIHPAKIGRGIMLDHATGIVGTAIVLENDVSTLHGVTG 222
 QY 223 GTGKQSGDRHPIKIGDVLIGAGSCITIGITTEGAKIGSGSVVKKDVPARTAVGNPRL 183
 DB 184 GTGKSGDRHPIKIGDVLIGAGSCITIGITTEGAKIGSGSVVKKDVPARTAVGNPRL 282
 QY 283 IGGKENPKRHDKTIPCLTMDQ 302
 DB 244 VGRKPS-----DK-PSMDMDQ 258

RESULT 2
 CYSE_SALTY
 ID CYSE_SALTY STANDARD; PRT; 273 AA.
 AC P29847;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 GN SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 OS *Salmonella typhimurium*.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC *Salmonella*.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RA SIVAPRASAD A.V., KUCZEK E.S., BAWDEN C.S., ROGERS G.E.;
 RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA ROGERS G.E.;

RT "Cysteine biosynthesis in transgenic animals."
 RL Patent number GB2227243, 25-JUL-1990.
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMODIMER. DIMER OF A HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC
 DR EMBL: X59594; CAA42163.1;
 DR EMBL: A00198; CAA00039.1;
 DR PIR: S29568; S29568.
 DR StyGene: SGI0073; CYSE.
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep. 2.
 DR PROSITE: PS00101; HEXAPEP-TRANSFERASES; 1.
 DR Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
 KW SEQUENCE 273 AA; 29291 MW; 6A5736E56FBD25B CRC64;
 SQ

Query Match
 Best Local Similarity 39.5%; Score 648.5; DB 1; Length 273;
 Matches 133; Conservative 50; Mismatches 72; Indels 5; Gaps 2;

DB 4 EELEIYWNKIKAEKADVKOEPIISNYVYASITSHRSLSALAHILSVKLSNLPNTL 102
 QY 103 FELFIVLEESSEITESTKODLAVKERDPACISYHCEFLGKFGFLACQARHATHTLMO 63
 DB 64 REVEEAVAADEPMASACDIOAVTRDPADVAKYSTPLLYLKFFHALQVYRGHMLNK 162
 QY 163 NRKIYALLIQNRSEFAVDIHGKATIGKGLLDHAGVVGTAAGVNDVSTLHGVTG 123
 DB 124 GRALALFQNOVSFQVDIHPAKIGRGIMLDHATGIVGTAIVLENDVSTLHGVTG 222
 QY 223 GTGKQSGDRHPIKIGDVLIGAGSCITIGITTEGAKIGSGSVVKKDVPARTAVGNPRL 183
 DB 184 GTGKSGDRHPIKIGDVLIGAGSCITIGITTEGAKIGSGSVVKKDVPARTAVGNPRL 282
 QY 283 IGGKENPKRHDKTIPCLTMDQ 302
 DB 244 VGRKPS-----DK-PSMDMDQ 258

RESULT 3
 CYSE_HAEM
 ID CYSE_HAEM STANDARD; PRT; 267 AA.
 AC P43886;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 GN SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 OS *Haemophilus influenzae*.
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 CC *Haemophilus*.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RA MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

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FR [1] SEQUENCE FROM N.A.
RC STRAIN= TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "genome sequence of the endocellular bacterial symbiont of aphids
RL Buchnera sp. APS."
RL Nature 407:81-86(2000).
CC -1- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = CoA + O-acetyl-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/PPX/NDOL FAMILY OF
CC ACETYLTRANSFERSES. COMPOSD OF MULTIPLE REPEATS OF [LIV]-G-X(4) .
CC
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CC
CC
CC EMBL: AF001118; BAB12777.1;
CC DR PROSITE: P500101; HEXAPEP_TRANSFERSES: 1.
CC TR: transferase: Acyltransferase; Cysteine biosynthesis; Repeat.
CC K: 274 AA; 30165 MW; 55305252P1048B6B1 CMC64;
CC SEQUENCE

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	Query Match	34.9%	Score 573.5;	DB 1;	Length 274;	
	Best Local Similarity	48.9%	Pred. No. 2,6e-38;			
	Matches 116;	Conservative	47;	Mismatches 73;	Indels 1;	Gaps
Oy	48	VWIMLEAKSDVKQPELTISNYVASTSHSLTESALAHLSYKLSNLNLPDNLFLFELI	107			
Ddb	9	IWNKLVDVSFLTKKEPLIDSPFOYSIOHOSFTSSLSYLTSNKRTSMTSEKKTIGLFD	68			
Oy	108	SYLEESPETESTRKODILAVKERDPACISYYHCFLGFKGLACQARRIAHTMKNKRIV	167			
Ddb	69	DVYLNDRLSTLFVIQDIKAVLKRDPAVNDDYLPFLTYLTKGHALEAARISHYLMNNGKSL	128			
Oy	168	ALLIONRSEFAVDIHFGAKIKSGILLDHANGVIGETAVAGDNVISLHGVLGGTGRO	227			
Ddb	129	SYLDSTRISSESVDHPAPAFISGVMDLHAHGVIIGEGVFTEEDNSVILSVTLGGTGKN	188			
Oy	228	-SGDRHKPIGDGVLVLAGSCILNTITGEGAKIGSGVVVDVPARTAVGNPARI	283			
Ddb	189	FQSNRHPTIRKGVGVIAGAGATLGNIENVEGSKATIGASIVLNKPVDYTVVGPAKIV	245			
	RESULT 5					
ID	CYSE_BUCAP	STANDARD;	PRT;	261 AA.		
AC	P32003;					
DT	01-JUL-1993 (Rel. 26, Created)					
DT	01-JUL-1993 (Rel. 26, Last sequence update)					
DT	30-MAY-2000 (Rel. 39, Last annotation update:					
DE	SERINE ACETYLTTRANSFERASE (EC 2.3.1.30) (SAT)					
CN	CYSE.					
OS	Buchnera aphidicola (subsp. Schizaphis graminum).					
OC	Bacteria; Proteobacteria; gamma subphylum; buchnera.					
OX	NCBL_TrxID=98794;					
RN	(1)					
RP	SEQUENCE FROM N.A.					
RA	MEDLINE=93012960; PubMed=1398077;					
RX	Lai C.-Y., Bauman P.;					
RT	*Sequence analysis of a DNA fragment from Buchnera aphidicola (an					
RT	endosymbiont of aphids) containing genes homologous to daag, rpoD,					
RT	rpoE, and secB.*;					
RL	Gene 119:113-118(1992).					
CC	-1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE -> COA + O-ACETYL-L-					
CC	SERINE.					
CC	-1- PATHWAY: CYSTEINE BIOSYNTHESIS.					

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC EMBL: M90644; AAA73232.1;
 DR EMBL: JCI293; JCI293;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep; 2.
 DR PROSITE: PS00101; HEXAPEP. TRANSFERASES; 1.
 DR TRANSFERASE: Acyltransferase; Cysteine biosynthesis; Repeat.
 KW TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
 SQ SEQUENCE 261 AA; 28914 MW; DC02685464A25944 CRC64.

Query Match
 Best Local Similarity 33.58; Score 549.5; DB 1; Length 261;
 Matches 109; Conservative 53; Mismatches 84; Indels 1; Gaps 1;
 QY 47 DWIKLEAKSDVYKOEPIISNYYSITSHRLESALHILSVKLSNLPSTLFLF 106
 DB 8 ELNNIKRKAOKIKKEPIISNYYSITSHRLESALHILSVKLSNLPSTLFLF 106
 QY 107 ISVLESEPIESTKODLIVKERRDPACTSYVHCEFGFGLACQAHRIATLTKONKI 166
 DB 68 NKIYANNISIIISVYKDIKAKASQSDPVVYKHYLPLLYLKPHALEYVLSHYLNIRYE 127
 QY 167 VALIQRNVESEPAVDIHPGAKIGKGIILDHATGVIGETAVGDNVSIHLGVLGCTG 226
 DB 128 LSAVLOSRISTVSVIHPAASIGSIMIDHATGVIGETAVGDNVSIHLGVLGCTG 226
 QY 227 QSG-DRHPRKTIGDVLIGAGSCITLNTTIGEGAKIGSGSVVYKDVDPARTVAGNPARLIG 285
 DB 188 NTGKNRPIIRKNTVITGAGAKILNIEVGQGVKAGSIVLKNIPPTVYVGPAAIKK 247
 QY 286 KENPRH 292
 DB 248 IKNSKN 254

RESULT 6
 CYSE_SYN7
 ID CYSE_SYN7 STANDARD; PRT; 244 AA.
 AC 056002;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE.
 OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96281517; PubMed=8661945;
 RA Anandan S., Nally M.S., Cogdell D.E., Golden S.S.;
 RT Identification of two classes of transcriptional regulator genes in
 RL the cyanobacterium Synechococcus sp. strain PCC 7942.
 RL Arch. Microbiol. 166:58-63(1996).
 CC -1- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC EMBL: I41665; AAB8543.1;
 DR EMBL: JCI293; JCI293;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep; 2.
 DR PROSITE: PS00101; HEXAPEP. TRANSFERASES; 1.
 DR TRANSFERASE: Acyltransferase; Cysteine biosynthesis; Repeat.
 KW TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
 SQ SEQUENCE 244 AA; 26453 MW; AB050491023ENBI CRC64.

Query Match
 Best Local Similarity 26.28; Score 430.5; DB 1; Length 244;
 Matches 85; Conservative 33; Mismatches 56; Indels 3; Gaps 1;
 QY 123 DLIANKDPACISYVHCEFGFGLACQAHRIATLTKONKIYALLIONRSESPAVD 182
 DB 8 DERIFERDPAARNGLEVLLCYPGQALVCHRYAHLVQKUPVPRLLSHLRLTGE 67
 QY 183 IHPGAKIGKGIILDHATGVIGETAVGDNVSIHLGVLGCTGQSGDRPKIGDVLG 242
 DB 68 IHPGARLGQGIIFLDHMGVIGETAVGDNVSIHLGVLGCTGQSGDRPKIGDVLG 242
 QY 243 AGSCITLNTTIGEGAKIGSGSVVYKDVDPARTVAGNPARLIG 296
 DB 128 AGAVLGNIDIGENRIVIGAGSVLVDVSDCTVYGIIFGRVIVSGVAVDPDLDSQMP 184

RESULT 7
 CYSE_BACSU
 ID CYSE_BACSU STANDARD; PRT; 217 AA.
 AC 006750;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE OR CYSA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94171772; PubMed=7510287;
 RA Gagnon Y., Breton R., Putzer H., Pelchat M., Grunberg-Manago M.,
 RA Lapointe J.;
 RT Clustering and co-transcription of the Bacillus subtilis genes
 RT encoding the aminocyl-tRNA synthetases specific for glutamate and
 RT for cysteine and the first enzyme for cysteine biosynthesis.
 RL J. Biol. Chem. 269:7473-7482(1994).
 CC -1- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODI FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4) .
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CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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-----
DR EMBL: D13777; BAA02919.1; -.
DR EMBL: D90912; BAI8167.1; -.
DR InterPro: IPR001451; -.
DR Pfam: PF00132; hexapep; 3.
DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
KW Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
FT CONFLICT 80 80 I -> S (IN REF. 1).
SQ SEQUENCE 249 AA; 27336 MW; ED5ECS8D659DCFB CRC64;
-----
Query Match 25.6%; Score 420.5; Dh: 1; Length 249;
Best Local Similarity 44.6%; Pred. No. 2.8e-26;
Matches 82; Conservative 35; Mismatches 64; Indels 3; Gaps 1;
-----
QY 116 IIESTKODLVAKERDPACISVHCFLEGFGLCAQHRAHTLMKNRKIVALLIQNRY 175
Db 1 MLNLSLADEFRIIFRPPDPARNWLEVLFCFYPGLQALLIHRSFLRYTLGLPFPRIMSHLA 60
QY 176 SESRAVDIHHPAKIGKGILLDHATGVYIGETAVYGDNVSLHGVTLLGSTGSGSDRHKI 235
Db 61 RFFGIIEHPAQIQGGQFYFDHGMGVYIGETAIVGDVSLIOGVTLTGSTGESGRHPTL 120
QY 236 GDGVLLICAGSCILLNTITGEGAKTIGSSGVYVKDVPAARTAVGNPARLI---GGENPKKH 292
Db 121 GENVVVGAGKAVLCNIATIGNVRIGAGSVLVLPADFTVGVGPGRMVPSPSERVNPLEH 180
QY 293 DKIP 296
Db 181 GKLP 184
-----
RESULT 9
CYSE_STAXY ID CYSE_STAXY STANDARD; PRT; 216 AA.
AC P77985;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAV).
GN CYSE.
OS Staphylococcus xylosus.
OC Bacteria; Firmicutes; Bacillus/Clostridium g. sp;
OC Bacillus/Staphylococcus group; Staphylococcus;
OX NCBI_TaxID=1288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 20267 / CZA.
RX MEDLINE=97237691; Pubmed=9084146;
RA Flegler H., Brueckner R.;
RT "Identification of the serine acetyltransferase gene of staphylococcus
RT xylosus".
RL FEBS Microbiol. Lett. 148:181-187(1997).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODI FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4) .
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EMBL: U43917; AAB07027.1; -
EMBL: AE000626; AAD08254.1; -
DR TIGR; HPI210; -
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep; 2.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
KW Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
FT VARIANT 5 5 S -> F (IN STRAIN 60190).
FT VARIANT 110 110 K -> R (IN STRAIN 60190).
FT VARIANT 162 162 S -> T (IN STRAIN 60190).
SQ SEQUENCE 171 AA; 18342 MW; 28646d539c2250c3 CRC64;

Query Match 22.2%; Score 365; DB 1; Length 171;
Best Local Similarity 45.2%; Pred. No. 4.1e-22;
Matches 71; Conservative 31; Mismatches 55; Indels 0; Gaps 0;

QY 127 VKERDPACISYVHCFGLGKFLGACQAHRIAHITLTKONRKIVALLIONRVSESPAVDHPG 186
DB 11 VLQEDPPAARNKWEVLLPYGTHALCYRLAHHLKRRFYIAIALSOLARFTGIEIHFG 70
QY 187 AKIGKILLDHATGVIGETAVGDNVSIHGVTLGSTGSGDRHPKIGDGVLIAGSGC 246
DB 71 AKIGKGLFIDHGMGVIGETGIDVDYIYHGVTLGSTGKFKGRHPTLGNRVVVGAGAK 130
QY 247 ILGNITIGEGAKIGSGSVVVDVARTTAVGNPARLI 283
DB 131 VLGAICVGDVRIKANAVVLSLPTGSTAVGSKAKTI 167

RESULT 12
CYSE_HELPJ STANDARD: PRT; 171 AA.
AC 092K14;
DT 01-OCT-2000 (Rel. 40; Created)
DT 01-OCT-2000 (Rel. 40; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE SERINE ACETYLTTRANSFERASE (EC 2.3.1.30) (SAT).
GN CYSE OR JHP1133.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
ON NCBI_TaxID=85963;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moll D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummato P.J., Caruso A., Ulla-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori";
RL Nature 397:176-180(1999).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NOXL FAMILY OF
CC ACETYLTTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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EMBL: AE001541; AAD06715.1; -
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep; 4.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
KW Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
SQ SEQUENCE 171 AA; 18354 MW; 2872B7539C3AC14A CRC64;

Query Match 21.9%; Score 359; DB 1; Length 171;
Best Local Similarity 44.6%; Pred. No. 1.2e-21;
Matches 70; Conservative 31; Mismatches 56; Indels 0; Gaps 0;

QY 127 VKERDPACISYVHCFGLGKFLGACQAHRIAHITLTKONRKIVALLIONRVSESPAVDHPG 186
DB 11 VLQEDPPAARNKWEVLLPYGTHALCYRLAHHLKRRFYIAIALSOLARFTGIEIHFG 70
QY 187 AKIGKILLDHATGVIGETAVGDNVSIHGVTLGSTGSGDRHPKIGDGVLIAGSGC 246
DB 71 AKIGKGLFIDHGMGVIGETGIDVDYIYHGVTLGSTGKFKGRHPTLGNRVVVGAGAK 130
QY 247 ILGNITIGEGAKIGSGSVVVDVARTTAVGNPARLI 283
DB 131 VLGAICVGDVRIKANAVVLSLPTGSTAVGSKAKTI 167

RESULT 13
SRPH_SYNPT STANDARD: PRT; 319 AA.
AC 059967;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE SERINE ACETYLTTRANSFERASE, PLASMID (EC 2.3.1.30) (SAT).
GN SRPH.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Plasmid pANL.
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
ON NCBI_TaxID=1140;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=95327059; PubMed=7603442;
RA Nicholson M.L., Gaasenbeek M., Landenbach D.E.;
RT "Two enzymes together capable of cysteine biosynthesis are encoded on
RT a cyanobacterial plasmid";
RL Mol. Gen. Genet. 247:623-632(1995).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NOXL FAMILY OF
CC ACETYLTTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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Query Match 17.5%; Score 287; DB 1; Length 319;

8

1/013 MW; E2402F836F3EB3AD CRC64;

matches 32; conservative 24; mismatches 54; indels 10; gaps 4;

20 AIRVAHFCSVARRKNVLNNLWAPLLVLRITTECFEGYEIQAAATIGRRFTIHGAVV 79

80 INKNVAGDDE^TIRHGVTIGNRGADN-MACPHIGNGVELSANVIL^LGDITLGNNTV^GGAG 138

Db 139 SVVLDSVPDNALVGEKARV 158

NODL_RHLY	CMWARD	SEE
ID	NODL_RHLY	100

DT	01-AUG-1988 (Rel. 08, Last sequence update)
DT	01-THU-1994 (Rel. 00, Last sequence update)

Rhizobium leguminosarum (biovar viciae).

NCBI_TaxID=387;

RX MEDLINE=88246045; Pubmed=3132583;

Mol. Microbiol. 2:173-183(1988).

Canter Cremers H.C.J., Spaik H.P., Wilffies A.H.M., Pees F

Plant MOL. Biol. 13:163-174(1989).

Downie J.A.; MEDLINE=50138034; PubMed=2615659; A

RL Mol. Microbiol. 3:1649-1651(1989).
 CC -1- FUNCTION: ACETYLTRANSFERASE IMPLICATED IN THE O-ACETYLATION OF
 CC MOD FACTORS.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPYA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 CC -----
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 CC -----
 DR EMBL: X17557; CAA35590.1; -;
 DR EMBL: Y00548; CAA68625.1; -;
 DR PIR: S01039; S01039.
 DR PIR: S07000; S07000.
 DR InterPro: IPR001451; -;
 DR Pfam: PF00132; hexapep. 2.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASE; Repeat.
 KW Plasmid; Modulation; Transferase; Acyltransferase; Repeat.
 SQ SEQUENCE 190 AA; 20105 MW; 2ACAAE82D6EDF48C CRC64;

Query Match 10.0%; Score 164.5; DB 1; Length 190;
 Best Local Similarity 42.7%; Pred. No. 3.1e-06;
 Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3;
 OY 193 ILDHATGVVIGETAVVGDVNSIL-----HGVTLGGTGKOSGDRHRPKIGDGVVIGAGSCI 247
 DB 89 VILDYA-AVTIGDGTATGPAVQITADHPHDEQRQAGLQG--RPVSIGRHAWIGGAIL 146
 OY 248 LIGNITIGEGAKIGSGVVVKDVPARTAVGNPARLIGGKENPR 290
 DB 147 LPGAIVTIGDHAIVIGAGSVVTRDVPAGSTAMGNPARVKAAGRLPK 189

Search completed: August 21, 2001, 12:09:35
 Job time: 172 sec

